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Quantitative trait loci for male reproductive traits in beef cattle*

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Summary

The objective of the present study was to detect quantitative trait loci (QTL) for male reproductive traits in a half-sib family from a *Bos indicus* (Brahman) × *Bos taurus* (Hereford) sire. The sire was mated with MARC III (1/4 Hereford, 1/4 Angus, 1/4 Red Poll and 1/4 Pinzgauer) cows. Testicular traits were measured from 126 male offspring born in 1996 and castrated at 8.5 months. Traits analysed were concentration of follicle stimulating hormone in peripheral blood at castration (FSH), paired testicular weight (PTW) and paired testicular volume (PTV) adjusted for age of dam, calculated age at puberty (AGE), and body weight at castration (BYW). A putative QTL was observed for FSH on chromosome 5. The maximum *F*-statistic was detected at 70 cM from the beginning of the linkage group. Animals inheriting the Hereford allele had a 2.47-ng/ml higher concentration of FSH than those inheriting the Brahman allele. Evidence also suggests the existence of a putative QTL on chromosome 29 for PTW, PTV, AGE and BYW. The maximum *F*-statistic was detected at cM 44 from the beginning of the linkage group for PTW, PTV and AGE, and at cM 52 for BYW. Animals that inherited the Brahman allele at this chromosomal region had a 45-g heavier PTW, a 42-cm^3 greater PTV, a 39-day younger AGE and a 22.8-kg heavier BYW, compared with those inheriting the Hereford allele. This is the first report of QTL for male reproductive traits in cattle.

Keywords genetic markers, male reproduction, quantitative trait, reproductive traits.

Reproductive development is directly related with fertility. Differences in testicular size, sperm production and age at puberty have been studied between *Bos taurus* and *Bos indicus* (Lunstra & Cundiff 2003). Thus, there is a need to characterize reproductive traits in males and to identify the genetics involved with the expression of these traits. The objective of the present study was to detect quantitative trait loci (QTL) for male reproductive traits in offspring from a *Bos indicus* × *Bos taurus* sire.

A half-sib family was developed using one Brahman × Hereford sire. The sire was mated with MARC III (1/4 Hereford, 1/4 Angus, 1/4 Red Poll and 1/4 Pinzgauer) cows in 1996 to produce 259 offspring, of which 126 were males. Calves were weaned at an average of 187 days and raised from weaning to castration on a corn–corn silage diet. Males were castrated at an average of 250.4 ± 0.7 days of age (8.5 months).

Blood samples were collected and leucocytes harvested from each bull. Plasma (5 cc) from each bull was retained for subsequent assay of serum FSH using a radioimmunoassay (RIA) validated for bovine FSH (Echternkamp *et al.* 2004).

Body weight, scrotal circumference and testicular length *in situ* were obtained for each bull, using procedures described by Lunstra *et al.* (1988). Age at puberty was calculated as the age (days) that each bull would have achieved a scrotal circumference of 28.0 cm by Lunstra *et al.* (1988). Average testicular length and width were used to calculate paired testicular volume employing the following formula (Young *et al.* 1986):

$$\mathrm{PTV} = 2\left[\frac{4}{3}\pi\left(\frac{1}{2}\mathrm{length}\right)\left(\frac{1}{2}\mathrm{width}\right)^2\right]$$

Paired testicular weight and paired testicular volume were also adjusted by age of dam, according to the procedure outlined by Lunstra *et al.* (1988).

Traits evaluated were age at puberty adjusted for age of dam (AGE), paired testicular weight adjusted for age of dam (PTW) and paired testicular volume (PTV) adjusted for age of dam (Lunstra *et al.* 1988), serum FSH concentration in

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peripheral blood at castration (FSH), and body weight at castration (BYW). Mean values and standard errors are shown in Table 1.

Table 1 Mean values and standard errors of evaluated traits.

Trait	Mean ± SE
FSH (ng/ml)	5.94 ± 0.33
PTW (g)	215.8 ± 6.3
PTV (cm^3)	186.7 ± 5.7
AGE (days)	345 ± 6
BYW (kg)	286.8 ± 2.8

FSH, concentration of follicle stimulating hormone in peripheral blood at castration; PTW, paired testis weight adjusted for age of dam; PTV, paired testis volume adjusted for age of dam; AGE, calculated age at puberty; BYW, body weight at castration.

Table 2 Chromosome, markers and their relative position in the linkage group used to detect putative QTL on chromosomes 5 and 29.

Chromosome	Marker	Relative position (cM)
5	*BMS1095*	0.0
	RM103	28.6
	BMC1009	40.6
	BR2936	64.3
	CSSM022	72.4
	BMS1216	75.6
	RM029	78.4
	BMS1248	88.4
	BMS597	120.0
29	*BMC2228*	0.0
	BMC8012	19.7
	BL1100	46.6
	RM389	55.2
	BMC6004	57.9
	BMS1948	61.6
	ILSTS081	65.0

A total of 130 markers were used in the analysis for this study. Amplification reactions were performed with purified DNA extracted from blood with a saturated salt procedure (Miller *et al.* 1988). Amplification conditions have been described elsewhere (Kappes *et al.* 1997).

An *F*-statistic profile was generated at 1 cM intervals for each chromosome. Data were analysed using the approach suggested by Haley *et al.* (1994). The model for FSH and BYW included age of dam as a fixed effect and age at castration as a covariate. The model for PTW, PTV and AGE, included only the effect of age at castration as a covariate. The conditional probability of inheriting the Brahman allele from the sire at each centimorgan was also incorporated as a covariate. The conditional probabilities of inheriting the Brahman allele were calculated with a FORTRAN program. The analysis for each chromosome was generated using the GLM procedure from SAS (SAS Inst. Inc., Cary, NC, USA). The 1-LOD drop-off method was used to calculate a support interval for each putative QTL (Ott 1992). An *F*-statistic was considered suggestive of linkage if it exceeded a value of $F = 10.4$ ($P = 0.002$; Lander & Kruglyak 1995).

Two chromosomal regions, one on chromosome 5 and the other on chromosome 29, showed evidence for the existence of putative QTL for male reproductive traits. Markers used and their relative positions within each linkage group are indicated in Table 2. A putative QTL for FSH was detected on chromosome 5, and putative QTL for PTW, PTV, AGE and BYW were identified in the telomeric region of chromosome 29. Table 3 shows the relative position of the maximum *F*-statistic, the support interval, the maximum *F*-statistic and the allelic effect.

Several studies have reported the presence of QTL for ovulation rate or twinning rate in cattle chromosome 5. Lien *et al.* (2000) detected a QTL for twinning rate between markers BL37 and BM1819. Cruickshank *et al.* (2004) detected a similar putative QTL for twinning rate on chromosome 5, between 63 and 90 cM. Kappes *et al.* (2000)

Table 3 Relative position, support interval and allelic effects of putative QTL detected with a suggestive threshold.

Chromosome	Trait	Relative position (cM)[1]	Support interval (cM)[1]	Effect (B–H)[2]	F[3]	P[4]	P[5]
5	FSH	70	47–82	−2.47	11.9	0.0008	0.54
29	PTW	44	38–46	44.7	12.2	0.0006	0.48
	PTV	44	37–46	41.8	13.0	0.0004	0.34
	AGE	44	34–57	−39.0	10.9	0.001	0.81
	BYW	52	37–59	22.8	16.0	0.0001	0.10

FSH, concentrations of follicle stimulating hormone in peripheral blood at castration; PTW, paired testis weight adjusted for age of dam; PTV, paired testis volume adjusted for age of dam; AGE, calculated age at puberty; BYW, body weight at castration.

[1]cM, relative position in centimorgans from the beginning of the linkage group.

[2]B, Brahman; H, Hereford (positive value implies Brahman had a greater effect than Hereford; negative value implies Hereford had a greater value than Brahman).

[3]Maximum *F*-statistic in the interval.

[4]Probability of false-positive for a single test.

[5]Expected number of false-positive per scan (Lander & Kruglyak 1995).

reported a QTL for ovulation rate in this chromosome. The position of the QTL in the three studies is similar to the position where the QTL for FSH in the present study was detected. If the QTL for ovulation rate in females and the QTL for FSH in males are caused by a single gene, then the mechanism behind the QTL for ovulation rate is possibly related to regulation of FSH in the female with a similar effect on FSH expression in males.

Bos indicus breeds exhibit reduced testicular size when compared with *Bos taurus* breeds (Lunstra & Cundiff 2003). The effect of the QTL detected on BTA29 in the present study indicates that offspring inheriting the Brahman allele had heavier testicular weight and greater testicular volume when compared with offspring inheriting the Hereford allele.

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